



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 22, 2026 – 06:09 PM JST

PDB ID : 9VAL / pdb_00009val
Title : Crystal structure of the PDZ tandem of syntenin
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Deposited on : 2025-06-03
Resolution : 2.15 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

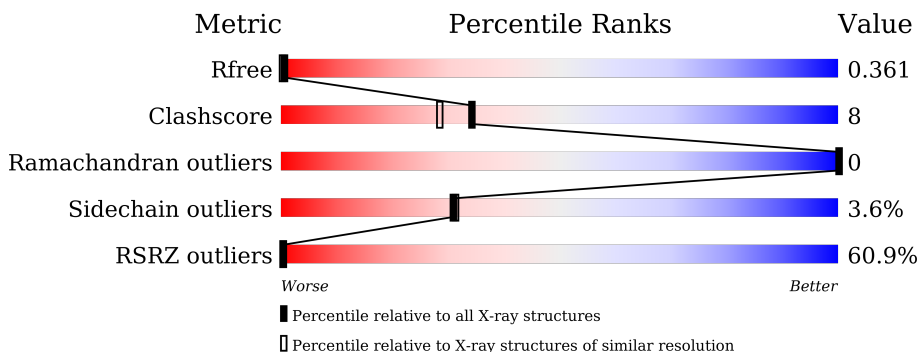
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2057 (2.16-2.16)
Clashscore	190562	2159 (2.16-2.16)
Ramachandran outliers	187476	2134 (2.16-2.16)
Sidechain outliers	187428	2133 (2.16-2.16)
RSRZ outliers	180081	2059 (2.16-2.16)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	166	<div> <div>62%</div> <div> <div></div> <div>80%</div> <div>18%</div> <div>..</div> </div> </div>
1	B	166	<div> <div>59%</div> <div> <div></div> <div>80%</div> <div>19%</div> <div>.</div> </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2531 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Syntenin-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	164	Total	C	N	O	S	0	0	0
			1248	783	223	236	6			
1	B	166	Total	C	N	O	S	0	0	0
			1270	797	225	242	6			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	275	TYR	PHE	engineered mutation	UNP O00560
B	275	TYR	PHE	engineered mutation	UNP O00560

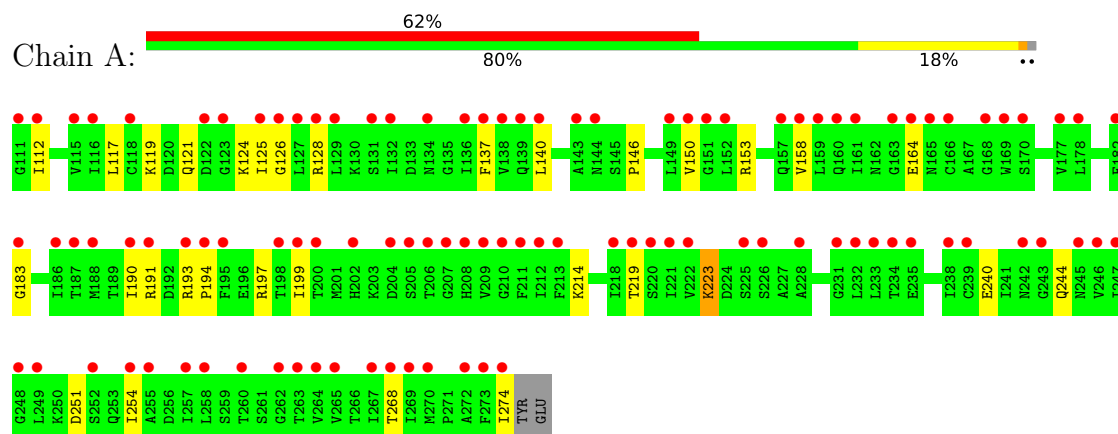
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	7	Total	O	0	0
			7	7		
2	B	6	Total	O	0	0
			6	6		

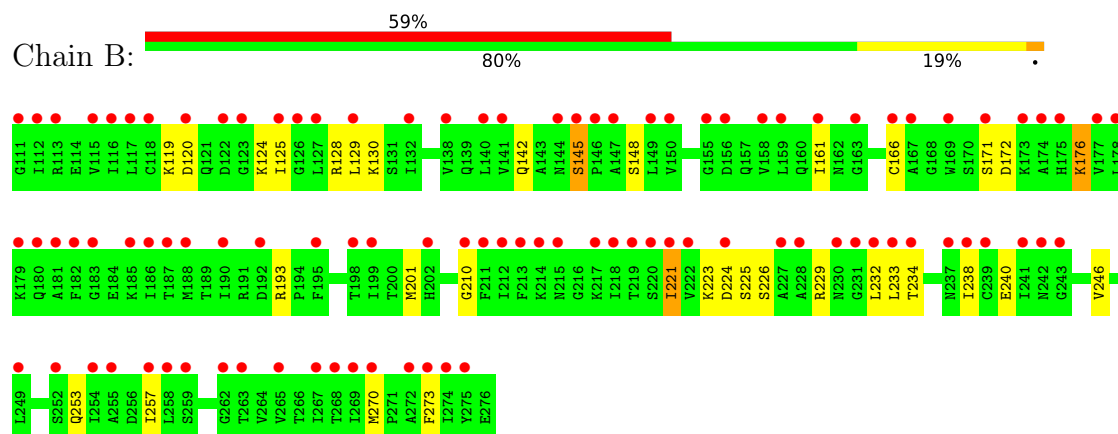
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Syntenin-1



• Molecule 1: Syntenin-1



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	56.88Å 56.88Å 149.20Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	46.78 – 2.15 46.78 – 2.15	Depositor EDS
% Data completeness (in resolution range)	100.0 (46.78-2.15) 95.3 (46.78-2.15)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.05 (at 2.16Å)	Xtriage
Refinement program	PHENIX 1.21.2_5419	Depositor
R, R_{free}	0.304 , 0.361 0.304 , 0.361	Depositor DCC
R_{free} test set	789 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	41.7	Xtriage
Anisotropy	0.487	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 43.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.39$, $\langle L^2 \rangle = 0.21$	Xtriage
Estimated twinning fraction	0.105 for -h,-k,l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	2531	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.96% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.10	0/1263	0.28	0/1700
1	B	0.17	0/1286	0.40	0/1730
All	All	0.14	0/2549	0.34	0/3430

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1248	0	1285	19	0
1	B	1270	0	1300	21	0
2	A	7	0	0	0	0
2	B	6	0	0	1	0
All	All	2531	0	2585	39	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

All (39) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:124:LYS:HD3	1:A:125:ILE:H	1.55	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:240:GLU:HB3	1:A:268:THR:HB	1.75	0.69
1:B:201:MET:HE1	1:B:232:LEU:HD22	1.77	0.66
1:A:124:LYS:HD2	1:A:126:GLY:H	1.64	0.61
1:A:197:ARG:HH22	1:A:199:ILE:HD11	1.67	0.59
1:B:119:LYS:HZ2	1:B:124:LYS:HA	1.69	0.58
1:B:119:LYS:NZ	1:B:124:LYS:HA	2.20	0.57
1:A:214:LYS:HB3	1:A:219:THR:HG21	1.87	0.57
1:B:225:SER:O	1:B:229:ARG:HG3	2.08	0.53
1:A:191:ARG:HG2	1:A:194:PRO:HG3	1.90	0.52
1:A:153:ARG:HD2	1:A:193:ARG:HD2	1.92	0.52
1:A:117:LEU:HG	1:A:150:VAL:HG11	1.92	0.51
1:A:197:ARG:NH2	1:A:199:ILE:HD11	2.25	0.51
1:A:124:LYS:HD3	1:A:125:ILE:N	2.24	0.51
1:B:226:SER:HA	1:B:229:ARG:HE	1.76	0.50
1:A:223:LYS:HD3	1:A:223:LYS:H	1.76	0.50
1:A:128:ARG:HB2	1:A:140:LEU:HB3	1.93	0.50
1:B:172:ASP:O	1:B:176:LYS:HE2	2.11	0.50
1:B:270:MET:HE3	1:B:273:PHE:HE1	1.76	0.50
1:B:130:LYS:HZ2	1:B:171:SER:HB2	1.76	0.49
1:A:119:LYS:HG3	1:A:183:GLY:HA2	1.95	0.49
1:B:253:GLN:O	1:B:257:ILE:HG13	2.13	0.49
1:B:238:ILE:HG22	1:B:246:VAL:HG21	1.95	0.48
1:B:119:LYS:HD3	1:B:125:ILE:HG22	1.97	0.47
1:A:158:VAL:HA	1:A:190:ILE:HG22	1.96	0.47
1:A:251:ASP:HA	1:A:254:ILE:HD12	1.97	0.47
1:B:210:GLY:HA3	1:B:225:SER:OG	2.14	0.47
1:B:221:ILE:HD11	1:B:234:THR:HG23	1.97	0.47
1:B:223:LYS:HA	1:B:223:LYS:HD2	1.67	0.45
1:B:142:GLN:HB3	1:B:145:SER:HB2	1.98	0.45
1:A:121:GLN:H	1:A:121:GLN:CD	2.27	0.43
1:A:146:PRO:O	1:A:150:VAL:HG13	2.19	0.43
1:B:193:ARG:NH2	2:B:301:HOH:O	2.51	0.42
1:B:193:ARG:HH12	1:B:240:GLU:CD	2.27	0.42
1:B:172:ASP:HB2	1:B:176:LYS:CE	2.50	0.41
1:B:161:ILE:HG13	1:B:166:CYS:SG	2.60	0.41
1:A:112:ILE:HD11	1:A:191:ARG:NH2	2.36	0.41
1:A:137:PHE:HZ	1:B:233:LEU:HD11	1.86	0.40
1:B:128:ARG:C	1:B:129:LEU:HD23	2.47	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	162/166 (98%)	157 (97%)	5 (3%)	0	100	100
1	B	164/166 (99%)	158 (96%)	6 (4%)	0	100	100
All	All	326/332 (98%)	315 (97%)	11 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	139/141 (99%)	135 (97%)	4 (3%)	37	39
1	B	141/141 (100%)	135 (96%)	6 (4%)	26	24
All	All	280/282 (99%)	270 (96%)	10 (4%)	31	31

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	164	GLU
1	A	223	LYS
1	A	244	GLN
1	A	274	ILE
1	B	120	ASP
1	B	145	SER
1	B	148	SER
1	B	176	LYS

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Mol	Chain	Res	Type
1	B	221	ILE
1	B	224	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	160	GLN
1	A	202	HIS
1	A	237	ASN
1	B	202	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	164/166 (98%)	2.28	103 (62%) 0 0	41, 59, 71, 77	0
1	B	166/166 (100%)	2.21	98 (59%) 0 0	42, 60, 81, 92	0
All	All	330/332 (99%)	2.24	201 (60%) 0 0	41, 60, 75, 92	0

All (201) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	222	VAL	5.2
1	B	238	ILE	4.8
1	B	140	LEU	4.5
1	A	267	ILE	4.4
1	A	247	ILE	4.4
1	B	237	ASN	4.2
1	A	161	ILE	4.1
1	A	274	ILE	4.0
1	B	272	ALA	4.0
1	A	116	ILE	3.9
1	A	258	LEU	3.9
1	A	234	THR	3.9
1	A	219	THR	3.9
1	A	213	PHE	3.8
1	A	115	VAL	3.8
1	B	227	ALA	3.8
1	A	165	ASN	3.7
1	B	129	LEU	3.7
1	A	210	GLY	3.7
1	A	186	ILE	3.7
1	A	239	CYS	3.7
1	B	125	ILE	3.7
1	B	178	LEU	3.6
1	B	254	ILE	3.6

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Mol	Chain	Res	Type	RSRZ
1	A	209	VAL	3.5
1	A	137	PHE	3.5
1	B	255	ALA	3.5
1	A	222	VAL	3.5
1	A	270	MET	3.5
1	B	265	VAL	3.5
1	B	150	VAL	3.5
1	A	144	ASN	3.4
1	B	177	VAL	3.4
1	B	182	PHE	3.4
1	A	199	ILE	3.4
1	A	212	ILE	3.4
1	A	231	GLY	3.3
1	A	221	ILE	3.3
1	A	112	ILE	3.3
1	B	199	ILE	3.3
1	B	267	ILE	3.3
1	A	138	VAL	3.2
1	B	181	ALA	3.2
1	A	152	LEU	3.2
1	B	117	LEU	3.2
1	A	195	PHE	3.2
1	A	194	PRO	3.2
1	A	140	LEU	3.1
1	B	241	ILE	3.1
1	B	243	GLY	3.1
1	A	136	ILE	3.1
1	A	238	ILE	3.1
1	B	171	SER	3.1
1	B	158	VAL	3.1
1	B	188	MET	3.1
1	B	123	GLY	3.0
1	A	200	THR	3.0
1	B	202	HIS	3.0
1	B	167	ALA	3.0
1	A	159	LEU	3.0
1	A	198	THR	3.0
1	B	195	PHE	3.0
1	B	228	ALA	3.0
1	A	272	ALA	2.9
1	A	249	LEU	2.9
1	A	265	VAL	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	138	VAL	2.9
1	B	213	PHE	2.9
1	A	254	ILE	2.9
1	A	242	ASN	2.9
1	A	126	GLY	2.9
1	B	233	LEU	2.8
1	A	263	THR	2.8
1	A	269	ILE	2.8
1	B	252	SER	2.8
1	A	255	ALA	2.8
1	B	224	ASP	2.8
1	B	239	CYS	2.8
1	B	269	ILE	2.8
1	B	169	TRP	2.8
1	B	147	ALA	2.7
1	A	178	LEU	2.7
1	B	127	LEU	2.7
1	B	275	TYR	2.7
1	B	175	HIS	2.7
1	B	174	ALA	2.7
1	B	232	LEU	2.7
1	B	132	ILE	2.7
1	A	207	GLY	2.7
1	A	211	PHE	2.6
1	A	149	LEU	2.6
1	A	232	LEU	2.6
1	B	249	LEU	2.6
1	B	141	VAL	2.6
1	B	186	ILE	2.6
1	A	260	THR	2.6
1	B	273	PHE	2.6
1	B	115	VAL	2.6
1	B	190	ILE	2.6
1	B	218	ILE	2.6
1	A	166	CYS	2.6
1	B	111	GLY	2.6
1	A	129	LEU	2.6
1	B	221	ILE	2.6
1	B	163	GLY	2.6
1	B	262	GLY	2.6
1	A	228	ALA	2.6
1	B	122	ASP	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	131	SER	2.6
1	A	273	PHE	2.5
1	B	180	GLN	2.5
1	A	164	GLU	2.5
1	A	177	VAL	2.5
1	B	258	LEU	2.5
1	A	169	TRP	2.5
1	A	150	VAL	2.5
1	A	183	GLY	2.5
1	A	262	GLY	2.5
1	B	185	LYS	2.5
1	A	191	ARG	2.5
1	A	125	ILE	2.5
1	A	205	SER	2.5
1	A	248	GLY	2.5
1	A	257	ILE	2.5
1	B	112	ILE	2.5
1	A	235	GLU	2.4
1	A	188	MET	2.4
1	B	217	LYS	2.4
1	B	210	GLY	2.4
1	B	144	ASN	2.4
1	B	230	ASN	2.4
1	B	156	ASP	2.4
1	B	268	THR	2.4
1	B	155	GLY	2.4
1	B	116	ILE	2.4
1	B	212	ILE	2.4
1	B	257	ILE	2.4
1	A	233	LEU	2.4
1	B	149	LEU	2.4
1	A	163	GLY	2.4
1	B	192	ASP	2.4
1	A	182	PHE	2.4
1	A	190	ILE	2.4
1	A	220	SER	2.4
1	B	263	THR	2.4
1	A	218	ILE	2.3
1	A	208	HIS	2.3
1	B	159	LEU	2.3
1	A	122	ASP	2.3
1	A	246	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	157	GLN	2.3
1	B	187	THR	2.3
1	A	193	ARG	2.3
1	A	204	ASP	2.3
1	B	231	GLY	2.3
1	A	225	SER	2.3
1	B	145	SER	2.3
1	A	160	GLN	2.2
1	B	211	PHE	2.2
1	A	206	THR	2.2
1	A	134	ASN	2.2
1	A	245	ASN	2.2
1	B	215	ASN	2.2
1	B	118	CYS	2.2
1	B	242	ASN	2.2
1	B	126	GLY	2.2
1	A	118	CYS	2.2
1	A	127	LEU	2.2
1	B	259	SER	2.2
1	A	132	ILE	2.2
1	B	146	PRO	2.2
1	A	151	GLY	2.2
1	A	168	GLY	2.2
1	A	143	ALA	2.2
1	A	128	ARG	2.2
1	B	113	ARG	2.2
1	A	187	THR	2.2
1	B	219	THR	2.2
1	B	234	THR	2.2
1	B	274	ILE	2.1
1	A	264	VAL	2.1
1	A	139	GLN	2.1
1	B	166	CYS	2.1
1	B	179	LYS	2.1
1	A	123	GLY	2.1
1	A	202	HIS	2.1
1	B	183	GLY	2.1
1	B	214	LYS	2.1
1	A	226	SER	2.1
1	B	270	MET	2.1
1	B	198	THR	2.1
1	A	111	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	161	ILE	2.1
1	B	173	LYS	2.1
1	A	252	SER	2.1
1	B	120	ASP	2.0
1	A	268	THR	2.0
1	A	243	GLY	2.0
1	A	158	VAL	2.0
1	A	170	SER	2.0
1	B	220	SER	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.